8. RNA

Program Name: RNA.java   Input File: rna.dat

You are taking an intro biology class, and you are learning about RNA transcription. In this process, an RNA strand must match up to an equal length DNA strand, as defined by the following matching.

At each position, a 'T' in the DNA strand must match with an 'A' in the RNA strand, an 'A' in the DNA strand must match with a 'U' in the RNA strand, a 'C' in the DNA strand must match with a 'G' in the RNA strand, or a 'G' in the DNA strand must match with a 'C' in the RNA strand. If these matchings occur at every position, the pair is deemed "good". If one or more positions are not matched, or any letters besides these occur, the pair is deemed "bad".

Your homework has a number of problems, each of which is checking whether a given DNA strand matches to a given RNA strand. However, your teacher has given you some strands of length up to 200! So, rather than spend forever on your homework, you write a program to do it for you.

Input
The first line will be a single integer T (< 10), the number of problems on your homework.
The first line of each problem will be a single integer N (0<=N<=200), the length of the strings for this problem. The following two lines will each contain a single string, each of length N. The first line will be the DNA strand, and the second line will be the RNA strand.

Output
For each problem, output "GOOD" if the strings only consist of the letters A, T, G, C, and U, and each base pair is matched properly between the strands. If one of these is not true, output "BAD" instead.

Example Input File
```
3
4
ATGC
UACG
4
ATGC
CGUA
3
AGQ
UCF
```
Example Output to Screen
```
GOOD
BAD
BAD
```

Explanation: In the first case, all 4 indexes are valid pairs, so the answer is good.
In the second case, the first pair, A-C is not valid, so the answer is bad.
In the third case, the last pair, Q-F, is not valid, so the answer is bad.